E26 DNA Mixture Interpretation: History, Challenges, Statistical Approaches, and Solutions

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After attending this presentation, attendees will better understand the DNA mixture interpretation approaches used in forensic DNA laboratories today.

This presentation will impact the forensic science community by helping the legal community appreciate laboratory difficulties with DNA mixture interpretation.

Since its introduction in the mid-1980s, forensic DNA testing has played an important role in the criminal justice community through aiding conviction of the guilty and exoneration of the innocent. New technologies are regularly introduced and validated to expand the capabilities of laboratories working to recover DNA results with improved sensitivity and informativeness. One of the largest challenges today is coping with interpretation of complex mixtures and low-level DNA profiles where portions of the evidentiary profile may be missing and thus unavailable for comparison to reference profiles.

A brief history of the forensic DNA field will be provided with a review of approaches to DNA mixture interpretation. Due to the prevalence of mixtures in many forensic casework situations, multi-allelic Short Tandem Repeat (STR) markers will likely remain a primary workhorse for DNA analysis into the foreseeable future. The 2010 Autosomal STR Interpretation Guidelines from the Scientific Working Group on DNA Analysis Methods (SWGDAM) have led to protocol changes in many forensic DNA laboratories.[1] The role and limitations of stochastic thresholds that are commonly used with some statistical methods will be discussed. The 2010 SWGDAM guidelines were written with a focus on single-source and two-person mixtures, and limitations exist in applying some basic concepts to more complex mixtures. Lessons learned from NIST interlaboratory studies will be reviewed along with information available on the NIST STRBase website that relates to mixture interpretation (http://www.cstl.nist.gov/strbase/mixture.htm). Key literature references and other educational resources will also be discussed.

Several software programs enable statistical calculations to be performed with probabilistic genotyping and/or incorporating a probability of allele dropout. These approaches enable analysts to account for the possibility of missing data in complex or low-level evidentiary DNA profiles. In December 2012, the DNA Commission of the International Society of Forensic Genetics (ISFG) published recommendations on evaluation of STR typing results that include drop-out and/or drop-in using probabilistic methods.[2] Some examples will be shared to show the relevance of different approaches that can be taken when complex DNA profiles are present in evidentiary results.

References:

1. http://www.swgdam.org/Interpretation_Guidelines_January_2010.pdf
2. Gill, P., et al. (2012). DNA Commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods. *Forensic Science International: Genetics, 6,* 679-688. Available at http://www.isfg.org/Publication;Gill2012.

Forensic DNA, DNA Mixtures, Mixture Interpretation

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